

IN THE SEQUENCE LISTING

Please **replace** the Sequence Listing of record with the Substitute Sequence Listing attached hereto.



SEQUENCE LISTING

<110> MENE-SAFFRANE, Laurent  
ESQUERRE-TUGAYE, Marie-Thérèse  
FOURNIER, Joëlle  
BEFFA, Roland  
GROSJEAN-COURNOYER Marie-Claire

<120> LIPOXYGENASE OVEREXPRESSION IN PLANTS  
AND REDUCTION IN PLANT SENSITIVITY TO  
DISEASES AND TO ATTACKS FROM PATHOGENIC  
ORGANISMS

<130> A36097-PCT-USA-A 075188.0117

<140> US/10/731,642  
<141> 2003-12-08

<150> PCT/FR02/01943  
<151> 2002-06-06

<150> FR 01/07470  
<151> 2001-06-07

<150> FR 01/14358  
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<309> 1995-07-16

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Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp Pro  
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Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu Asn  
65 70 75 80

Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe Arg

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Val Thr Phe Asp Trp Asp Asp Glu Glu Phe Gly Val Pro Gly Ala Phe			
100	105	110	
Ile Ile Lys Asn Leu His Phe Ser Glu Phe Phe Leu Lys Ser Leu Thr			
115	120	125	
Leu Glu Asp Val Pro Asn His Gly Lys Val His Phe Val Cys Asn Ser			
130	135	140	
Trp Val Tyr Pro Ala Asn Lys Tyr Lys Ser Asp Arg Ile Phe Phe Ala			
145	150	155	160
Asn Gln Ala Tyr Leu Pro Ser Glu Thr Pro Asp Thr Leu Arg Lys Tyr			
165	170	175	
Arg Glu Asn Glu Leu Val Thr Leu Arg Gly Asp Gly Thr Gly Lys Leu			
180	185	190	
Glu Glu Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu Gly			
195	200	205	
Asp Pro Asp Lys Gly Gln Asp Leu Ser Arg Pro Val Leu Gly Gly Ser			
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Ser Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Lys Pro Thr			
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Lys Thr Asp Pro Asn Ser Glu Ser Arg Ile Pro Leu Leu Met Ser Leu			
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Asp Ile Tyr Val Pro Arg Asp Glu Arg Phe Gly His Ile Lys Leu Ser			
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275	280	285	
Glu Phe Lys Ala Leu Phe Asp Ser Thr His Asn Glu Phe Asp Ser Phe			
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Glu Asp Val Leu Lys Leu Tyr Glu Gly Gly Ile Lys Leu Pro Gln Gly			
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Glu Leu Leu Arg Ser Asp Gly Glu Gly Leu Phe Lys Tyr Pro Thr Pro			
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Gln Val Ile Gln Glu Asp Lys Thr Ala Trp Arg Thr Asp Glu Glu Phe			
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385 390 395 400  
Gln Asn Ser Thr Ile Thr Arg Glu Gln Ile Glu Asp Lys Leu Asp Gly  
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420 425 430  
His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser Thr  
435 440 445  
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450 455 460  
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Gly Asp Gln Phe Gly Ala Val Ser Lys Val Tyr Thr Pro Ala Asp Gln  
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Asn Asp Ser Gly Val His Gln Leu Ile Ser His Trp Leu Asn Thr His  
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Leu His Pro Ile Tyr Lys Leu Leu His Pro His Phe Arg Glu Thr Met  
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565 570 575  
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Val Val Tyr Lys Asp Trp Val Phe Pro Glu Gln Ala Leu Pro Thr Asp  
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Leu Ile Lys Arg Gly Val Ala Val Glu Asp Ser Ser Ser Pro Leu Gly  
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625 630 635 640  
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645 650 655  
Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala Trp  
660 665 670  
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675 680 685  
Trp Trp Pro Lys Met Gln Thr Val Gln Glu Leu Ile Asp Ser Cys Thr

690	695	700
Ile Thr Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly		
705	710	715
Gln Tyr Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Leu Ser Arg		
725	730	735
Asn Phe Met Pro Glu Pro Gly Ser Pro Glu Tyr Glu Glu Leu Lys Thr		
740	745	750
Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln Thr		
755	760	765
Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser Asp		
770	775	780
Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp Gln		
785	790	795
Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp Ile		
805	810	815
Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn Arg		
820	825	830
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 agcacgacac gcttgtctac tccaaaaata tcaaagatac agtctcagaa gaccaaaggg 180  
 caattgagac tttcaacaa aggtaatat ccggaaacct cctcggattc cattgcccag 240  
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 attgcataa aggaaaggcc atcggtgaag atgcctctgc cgacagtggt cccaaagatg 360  
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 cgcaagaccc ttcccttat aaggaagttc atttcatttg gagaggacac gcggtaccca 540  
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 gga aaa aag gta aaa gga aca gtg gtt ttg atg aag aaa aat gtt ttg 635  
     Gly Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu  
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 gat ttt act gat att aat gcc tca gtt ctt gat gga gtt ctt gag ttc 683  
     Asp Phe Thr Asp Ile Asn Ala Ser Val Leu Asp Gly Val Leu Glu Phe  
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 ctt ggt cgg agg gtc tct ctc gag ttg atc agt tct gtt aat gct gat 731  
     Leu Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp  
     50               55               60  
 cct gca aat ggt tta caa ggg aaa cgc agc aaa gca gca tat ttg gag 779  
     Pro Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu  
     65               70               75  
 aac tgg cta aca aat agc acc cca ata gca gca ggt gaa tca gca ttt 827  
     Asn Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe  
     80               85               90               95  
 aga gtc aca ttt gat tgg gat gat gag gaa ttt gga gtt cca gga gca 875  
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 ttc att atc aag aac ttg cat ttt agt gag ttc ttc ctc aag tca ctc 923  
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 acc ctt gaa gat gtt cct aat cat ggc aaa gtt cat ttt gtc tgt aat 971  
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     Ser Trp Val Tyr Pro Ala Asn Lys Tyr Lys Ser Asp Arg Ile Phe Phe  
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gcg aat cag gct tat cta cca agt gaa aca cca gac aca ttg cga aaa Ala Asn Gln Ala Tyr Leu Pro Ser Glu Thr Pro Asp Thr Leu Arg Lys 160 165 170 175	1067
tac aga gaa aat gaa tta acc tta aga gga gat gga act gga aag Tyr Arg Glu Asn Glu Leu Val Thr Leu Arg Gly Asp Gly Thr Gly Lys 180 185 190	1115
ctt gag gaa tgg gat aga gtt tat gac tat gct tac tac aat gac ttg Leu Glu Glu Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu 195 200 205	1163
ggt gat cca gac aaa ggc caa gat ttg tca agg cct gtc tta gga gga Gly Asp Pro Asp Lys Gly Gln Asp Leu Ser Arg Pro Val Leu Gly Gly 210 215 220	1211
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aac cat cat gat atc ctt atg cca tac ttg agg aga att aac acg tcg Asn His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser 435 440 445	1883
aca gac aca aaa acc tat gcc tca aga act ctg ctc ttc ttg caa gat Thr Asp Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp 450 455 460	1931
aat gga act ttg aag cca tca gca att gaa cta agc ttg cca cat cca Asn Gly Thr Leu Lys Pro Ser Ala Ile Glu Leu Ser Leu Pro His Pro 465 470 475	1979
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aaa att tgg tca gca att aaa agt tgg gta act gaa tac tgc aac tac		2507	
Lys Ile Trp Ser Ala Ile Lys Ser Trp Val Thr Glu Tyr Cys Asn Tyr			
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tat tac aaa tca gat gat gcg gtt caa aaa gac act gaa ctc caa gcc		2555	
Tyr Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala			
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Thr Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln			
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aca ctg ctt ggc att tcc ctc ata gag atc ttg tca agg cat tct tcg		2891	
Thr Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser			
770	775	780	
gat aca ctt tac ctc ggg caa agg gaa tca cct gaa tgg aca aag gat		2939	
Asp Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp			
785	790	795	
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Gln Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp			
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Ile Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn			
820	825	830	
agg tcg ggt cct gtt aaa gtt cca tac acc ttg ctc ttc ccc aca agt		3083	
Arg Ser Gly Pro Val Lys Val Pro Tyr Thr Leu Leu Phe Pro Thr Ser			

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gaa gga gga ctt act ggc aaa gga att cct aac agt gtg tca ata tag		3131
Glu Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile		
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gctatatattt gttttctatac gcgtattaaa tgtataattg cgggactcta atcataaaaa	3251	
cccatctcat aaataacgtc atgcattaca tgttaattat tacatgctta acgtaattca	3311	
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